DNA

A DNA strand is made up of nucleotides, with four types of nucleobases: A, T, G, and C. For example: 'AAAACCCGT'. The base pair of A is T, and the base pair of C is G. If a DNA strand has any other letter, it is considered an 'Invalid DNA'. Capitalized letters and non-capitalized letters are considered the same in this question. Please write a program that processes DNA strands.

Input

The first line is a string of a DNA strand.

The second line is the operator. There are three types of operators that can be accepted:

1) R: Reverse Complement. This operator changes each nucleotide into its base pair, then reverses the entire strand. For example: AAAACCCGGT is changed to TTTTGGGCCA, and then reversed to ACCGGGTTTT.

2) F: Displays the frequency of A, T, G, and C in that order. For example, AAAACCCGGT will return A=4, T=1, G=2, C=3. (Note that there is 1 space bar after the comma.)

3) D: Displays the number of times a pair shows up in the DNA strand. This operator will accept 1 additional input of the pair the user is interested in. For example, GC or AA. Note that GC isn't the same as CG, and the count is checked for every nucleotide, one at a time. For example, in AAAA, 3 pairs of AA will be counted.

Hint: You only have to check the input for Invalid DNA. All given operators are guaranteed to be correct. *** Don't forget to call strip() when accepting input() before processing it.

Output

The output may vary, depending on the chosen operator.

Note: The color of each nucleotide in the example is only for visibility.

Example

Input (from keyboard)	Output (on screen)
ATTTGCGGCATATCC R	GGATATGCCGCAAAT
ATTTGCGGCATATCC F	A=3, T=5, G=3, C=4
ATTTGCGGCATATCC D GC	2
ATTTGCGGCATATCC D TT	2
ATTTGCGGCANTATCC F	Invalid DNA
aTTTgcggCAtaTCC R	GGATATGCCGCAAAT